

SEQUENCE LISTING

<110> GALZI, JEAN-LUC
ALIX, PHILIPPE

<120> USE OF A FLUORESCENT PROTEIN FOR DETECTING INTERACTION
BETWEEN A TARGET PROTEIN AND ITS LIGAND

<130> 97AHCNRFLU

<140> 09/445,205
<141> 2000-01-07

<150> PCT/FR98/01136
<151> 1998-06-04

<150> FR 97/06977
<151> 1997-06-05

<160> 25

<170> PatentIn Ver. 2.1

<210> 1
<211> 798
<212> DNA
<213> Aequorea victoria

<220>
<221> CDS
<222> (1)...(795)

<400> 1
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag 240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

| | |
|---|-----|
| cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag | 336 |
| Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu | |
| 100 105 110 | |
| gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc | 384 |
| Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly | |
| 115 120 125 | |
| atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac | 432 |
| Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr | |
| 130 135 140 | |
| aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac | 480 |
| Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn | |
| 145 150 155 160 | |
| ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc | 528 |
| Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser | |
| 165 170 175 | |
| gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc | 576 |
| Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly | |
| 180 185 190 | |
| ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg | 624 |
| Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu | |
| 195 200 205 | |
| agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc | 672 |
| Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe | |
| 210 215 220 | |
| gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tac | 720 |
| Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Tyr | |
| 225 230 235 240 | |
| tca gat ctc gag ctc aag ctt cga att ctg cag tcg acg gta ccg cgg | 768 |
| Ser Asp Leu Glu Leu Lys Leu Arg Ile Leu Gln Ser Thr Val Pro Arg | |
| 245 250 255 | |
| gcc cgg gat cca ccg gat cta gat aac tga | 798 |
| Ala Arg Asp Pro Pro Asp Leu Asp Asn | |
| 260 265 | |
| <210> 2 | |
| <211> 265 | |
| <212> PRT | |
| <213> Aequorea victoria | |
| <400> 2 | |
| Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu | |
| 1 5 10 15 | |
| Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly | |
| 20 25 30 | |

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Tyr
 225 230 235 240

Ser Asp Leu Glu Leu Lys Leu Arg Ile Leu Gln Ser Thr Val Pro Arg
 245 250 255

Ala Arg Asp Pro Pro Asp Leu Asp Asn
 260 265

<210> 3
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: spacer sequence

<400> 3
 Gly Gly Gly Gly Ser
 1 5

<210> 4
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cyclopeptide

<400> 4
Gln Trp Phe Gly Leu Met
1 5

<210> 5
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 5
ggtcgccacc ctgtacaaga agggcgagg

29

<210> 6
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 6
cacgagagga tgtacaacct cgagcgacca gtcacc

36

<210> 7
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 7
gtacccagac accagcttagc agatctgaag cttcgccatc aggc

44

<210> 8
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
ggagagttcc aactcgagaa aagaaagaag ggcgaggag 39

<210> 9
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
gtcagctgtt tctgcggcgc gctaagcctg ggccctt 36

<210> 10
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 10
ttagttctaa actagcggcc gcactagtcc tccatgaaca cttcagcccc a 51

<210> 11
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
cttgaaccta tagcttagcct cgagtcagca ttggcgggag gg 42

<210> 12
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 12
cctgctgtct cagatctcat caccgtcc 28

<210> 13
<211> 47

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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide

<400> 13
cagatcattta gttgtacagg aaagatcttg aggatcctgg agtgaag 47

<210> 14
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
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<400> 14
ggcccaagct tatgtcagga tccggggat 29

<210> 15
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
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<400> 15
cgcccgctcg agtcacaagc ccacagatat 30

<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide

<400> 16
gttgacaagc ttccggatcc a 21

<210> 17
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide

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<400> 17
acacacagagg gcagtagcaa tgaggatgac agcgaggcgt gccgcggaga ctttcattgg 60
atcccgaaac ttgtcaac 78

<210> 18
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 18
attgctactg ccctctgtgc tcctgcatct gcctcccat attcctcgga caccacacca 60
tgctgcttcg cctacatt 78

<210> 19
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 19
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gtaggcgaag cagcatgg 78

<210> 20
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 20
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gtaggcgaag cagcatgg 78

<210> 21
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 21

ctagctcata tccagcgagt tgatgtactc ccgaacccat ttcttctctg ggttggcaca 60
 aacttgacg 69

<210> 22
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
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<400> 22
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<210> 23
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 23
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<210> 24
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
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<400> 24
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<210> 25
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide

<400> 25
 ccgctcgagt taatctagaa ggaccagatt gtactccttc agg 43